

Page 1 of 7  
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 TC 1000 MAIL ROOM

RAW SEQUENCE LISTING DATE: 08/02/2000  
 PATENT APPLICATION: US/09/147,443B TIME: 10:36:42

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3 <110> APPLICANT: Morell, Andreas  
 4 Imboden, Martin  
 5 Stadler, Beda  
 6 Miescher, Sylvia  
 7 Vogel, Monique  
 8 Amstutz, Hanspeter  
 10 <120> TITLE OF INVENTION: POLYPEPTIDES CAPABLE OF FORMING ANTIGEN BINDING  
 11 STRUCTURES WITH SPECIFICITY FOR THE RHESUS D ANTIGENS,  
 12 THE DNA ENCODING THEM AND THE PROCESS FOR THEIR  
 13 PREPARATION AND USE  
 15 <130> FILE REFERENCE: 6816/P63221US0  
 17 <140> CURRENT APPLICATION NUMBER: 09/147,443B  
 C--> 18 <141> CURRENT FILING DATE: 1998-12-24  
 20 <150> PRIOR APPLICATION NUMBER: PCT/EP97/03253  
 21 <151> PRIOR FILING DATE: 1997-06-20  
 23 <150> PRIOR APPLICATION NUMBER: EP 96810421.6  
 24 <151> PRIOR FILING DATE: 1996-06-24  
 26 <160> NUMBER OF SEQ ID NOS: 64  
 28 <170> SOFTWARE: PatentIn Ver. 2.1  
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 42 1 5 10 15  
 44 tcc ctg aga ctc tcc tgt ata gcg tct gga ttc acc ctc agg aat tat 96  
 45 Ser Leu Arg Leu Ser Cys Ile Ala Ser Gly Phe Thr Leu Arg Asn Tyr  
 46 20 25 30  
 48 gcc atg cac tgg gtc cgc cag gct cca ggc aag ggg ctg gag tgg gtg 144  
 49 Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 50 35 40 45  
 52 gca ggt ata tgg ttt gat gga agt aac aaa aac tat gca gac tcc gtg 192  
 53 Ala Gly Ile Trp Phe Asp Gly Ser Asn Lys Asn Tyr Ala Asp Ser Val  
 54 50 55 60  
 56 aag ggc cga ttc acc atc tcc aga gac aat tcc aag aac acg ctg tat 240  
 57 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
 58 65 70 75 80  
 60 ctg caa ctg aac agc ctg aga gac gag acg gct gtg tat tat tgt 288  
 61 Leu Gln Leu Asn Ser Leu Arg Asp Glu Asp Thr Ala Val Tyr Tyr Cys  
 62 85 90 95  
 64 gcg aga gag cga gca gca cgt ggt att tct agg ttc tat tac tac atg 336  
 65 Ala Arg Glu Arg Ala Ala Arg Gly Ile Ser Arg Phe Tyr Tyr Tyr Met

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83 20 25 30
85 Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
86 35 40 45
88 Ala Gly Ile Trp Phe Asp Gly Ser Asn Lys Asn Tyr Ala Asp Ser Val
89 50 55 60
91 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
92 65 70 75 80
94 Leu Gln Leu Asn Ser Leu Arg Asp Glu Asp Thr Ala Val Tyr Tyr Cys
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117 1 5 10 15
119 gtc acc atc act tgc cgg gca agt cag agc att agg agc cat ttg aat 96
120 Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Arg Ser His Leu Asn
121 20 25 30
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124 Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Gly
125 35 40 45
127 gcg tcc act ttg caa agt ggc gtc cca tca agg ttc agt ggc agt ggc 192
128 Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
129 50 55 60
131 tct ggg gca gtt ttc act ctc acc atc gcc agt cta caa cct gaa gat 240
132 Ser Gly Ala Val Phe Thr Leu Thr Ile Ala Ser Leu Gln Pro Glu Asp
133 65 70 75 80
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141      100      105
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154      20      25      30
156 Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Gly
157      35      40      45
159 Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
160      50      55      60
162 Ser Gly Ala Val Phe Thr Leu Thr Ile Ala Ser Leu Gln Pro Glu Asp
163      65      70      75      80
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185      1      5      10      15
187 tcc ctg aga ctc tcc tgt gaa gcg tct gga ttc gcc ctc aga agt tct
188 Ser Leu Arg Leu Ser Cys Glu Ala Ser Gly Phe Ala Leu Arg Ser Ser
189      20      25      30
191 ggc atg cac tgg gtc cgc cag gct cct ggc aag ggg ctg gag tgg gtg
192 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
193      35      40      45
195 gca ctt ata tgg ttt gat gga agt atc aga tcg tat gca gaa tcc gtg
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197      50      55      60
199 aag ggc cga ttc acc atc tcc aga gac act tcc aag aac acc cta tat
200 Lys Gly Arg Phe Thr Ile Ser Arg Asp Thr Ser Lys Asn Thr Leu Tyr
201      65      70      75      80
203 ctc caa atg cgc agt ctg agt gcc gac gac acg gct gtg tat tac tgt
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208 Ala Arg Asp Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met
209          100          105          110
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226 20 25 30
228 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
229 35 40 45
231 Ala Leu Ile Trp Phe Asp Gly Ser Ile Arg Ser Tyr Ala Glu Ser Val
232 50 55 60
234 Lys Gly Arg Phe Thr Ile Ser Arg Asp Thr Ser Lys Asn Thr Leu Tyr
235 65 70 75 80
237 Leu Gln Met Arg Ser Leu Ser Ala Asp Asp Thr Ala Val Tyr Tyr Cys
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262 gtc acc atc act tgc cgg gca agt cag aac att atc cgc tat tta aat 96
263 Val Thr Ile Thr Cys Arg Ala Ser Gln Asn Ile Ile Arg Tyr Leu Asn
264 20 25 30
266 tgg tat cag cag aag cca ggg aaa gcc cct agg ctc ctg atc tat ggt 144
267 Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile Tyr Gly
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270 gcg tcc act ttg caa agt ggg gtc cca tca agg ttc agt ggc agt gga 192
271 Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
272 50 55 60
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276 65 70 75 80
278 ttt gca act tac tac tgt caa cag agt tac cgt acc cct cca ttc act 288
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299 Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile Tyr Gly
300 35 40 45
302 Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
303 50 55 60
305 Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
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331 Ser Leu Arg Leu Ser Cys Glu Ala Ser Gly Phe Thr Leu Arg Ser Ser
332 20 25 30
334 ggc atg cac tgg gtc cgc cag gct cct ggc aag ggg ctg gag tgg gtg 144
335 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
336 35 40 45
338 gca ctt ata tgg ttt gat gga agt atc aga tcg tat gca gaa tcc gtg 192
339 Ala Leu Ile Trp Phe Asp Gly Ser Ile Arg Ser Tyr Ala Glu Ser Val
340 50 55 60
342 aag ggc cga ttc acc atc tcc aga gac act tcc aag aac acc cta tat 240
343 Lys Gly Arg Phe Thr Ile Ser Arg Asp Thr Ser Lys Asn Thr Leu Tyr

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